

Amendments to the Claims

1. (Currently Amended) An isolated and purified bacterial reverse transcriptase (RT) of ~~(SEQ ID NO: 1)~~, which synthesizes msDNA, ~~and which~~ wherein said RT further comprises:

1) a sequence of amino acid residues as follows: Tyr-Xaa₆-Asp-Asp of (SEQ ID NO: 50), wherein Xaa₆ is alanine or cysteine;

2) and further comprises a second sequence of amino acid residues as follows: Asn-Xaa₁-Xaa₂, wherein Xaa₁ is a hydrophobic residue selected from the group consisting of alanine, leucine, and phenylalanine, and Xaa₂ is a hydrophobic residue selected from the group consisting of leucine, valine, and isoleucine[.];

3) a third sequence of amino acid residues as follows: Ser-Xaa₃-Xaa₄-Xaa₅ of SEQ ID NO: 51, wherein Xaa₃ is a hydrophobic residue selected from the group consisting of valine, phenylalanine, leucine, and isoleucine, Xaa₄ is a polar residue selected from the group consisting of threonine, asparagine, lysine, and serine, and Xaa₅ is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine, and alanine;

4) a fourth sequence of amino acid residues as follows: Xaa₇-Val-Thr-Gly, wherein Xaa₇ is a polar residue selected from the group consisting of arginine, glutamic acid, valine, and glutamine, of SEQ ID NO: 52; and

5) a fifth sequence of amino acid residues as follows: Gly-Xaa₈-Pro, wherein Xaa₈ is selected from the group consisting of alanine, phenylalanine and serine.

2. - 6. (Canceled)

7. (Currently Amended) An isolated and purified bacterial reverse transcriptase (RT) which synthesizes msDNA and which is essential for the synthesis of msDNA *in vivo*, said RT comprises a sequence of amino acid residues as follows: Tyr- Xaa₆-Asp-Asp, wherein Xaa₆ is alanine or cysteine, as shown in SEQ ID NO: 50, wherein said sequence is located in subdomain 5 shown in Fig. 14 at positions 175-191 of SEQ ID NO: 32, at positions 175-191 of SEQ ID NO: 33, at positions 175-191 of SEQ ID NO: 34, at positions 168-184 of SEQ ID NO: 35, at positions 159-175 of SEQ ID NO: 36, at positions 171-187 of SEQ ID NO: 37, and at positions 157-173 of SEQ ID NO: 38, and further comprising the 61 amino acid residues as shown by black dots in Figure 14 of SEQ ID Nos: 32-28, wherein h is a hydrophobic residue and p is a small polar residue.

8. - 17. (Canceled)